



SEQUENCE LISTING

#10

<110> APPLICANTS:

- (A) Jobling, Stephen Alan
- (B) Safford, Richard

<120> TITLE OF INVENTION: Improvements in or Relating to Starch Content of Plants

<130> Case 1637

<140> US 09/297,703

<141> 1999-07-19

<150> PCT/GB97/03032

<151> 1997-11-04

<160> 36

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Phe Pro Cys Ala Pro Leu Cys Lys Ser Gln Ser Thr Gly Phe His Gly	
15 20 25	

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Tyr Arg Arg Thr Ser Ser Cys Leu Ser Phe Asn Phe Lys Glu Ala Phe	
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Asn Val Met Val Thr Ala Ser Lys Arg Val Leu Pro Asp Gly Arg Ile	
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Glu Cys Tyr Ser Ser Ser Thr Asp Gln Leu Glu Ala Pro Gly Thr Val	
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CAATTTTGTA TATATGCCAA CGAGGATTTT AAGTTTTAAA AAAAAACAA AAAAAATCCA	2911
--	------

TG	2913
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<210> SEQ ID NO: #29

<211> LENGTH: 837 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #29

Met Gly His Tyr Thr Ile Ser Gly Ile Arg Phe Pro Cys Ala Pro Leu  
1 5 10 15

Cys Lys Ser Gln Ser Thr Gly Phe His Gly Tyr Arg Arg Thr Ser Ser  
20 25 30

Cys Leu Ser Phe Asn Phe Lys Glu Ala Phe Ser Arg Arg Val Phe Ser  
35 40 45

Gly Lys Ser Ser His Glu Ser Asp Ser Ser Asn Val Met Val Thr Ala  
50 55 60

Ser Lys Arg Val Leu Pro Asp Gly Arg Ile Glu Cys Tyr Ser Ser Ser  
65 70 75 80

Thr Asp Gln Leu Glu Ala Pro Gly Thr Val Ser Glu Glu Ser Gln Val  
85 90 95

Leu Thr Asp Val Glu Ser Leu Ile Met Asp Asp Lys Ile Val Glu Asp  
100 105 110

Glu Val Asn Lys Glu Ser Val Pro Met Arg Glu Thr Val Ser Ile Arg  
115 120 125

Lys Ile Gly Ser Lys Pro Arg Ser Ile Pro Pro Pro Gly Arg Gly Gln  
130 135 140

Arg Ile Tyr Asp Ile Asp Pro Ser Leu Thr Gly Phe Arg Gln His Leu  
145 150 155 160

Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu Arg Glu Glu Ile Asp Lys  
165 170 175

Tyr Glu Gly Ser Leu Asp Ala Phe Ser Arg Gly Tyr Glu Lys Phe Gly  
180 185 190

Phe Ser Arg Ser Glu Thr Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly  
195 200 205

Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe Asn Asn Trp Asn Pro Asn  
210 215 220

Ala Asp Val Met Thr Gln Asn Glu Cys Gly Val Trp Glu Ile Phe Leu

225		230		235		240
Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro His Gly Ser Arg Val						
	245			250		255
Lys Ile Arg Met Asp Thr Pro Ser Gly Asn Lys Asp Ser Ile Pro Ala						
	260			265		270
Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu Leu Pro Tyr Asn Gly						
	275			280		285
Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr Val Phe Lys Asn Pro						
	290			295		300
Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Ser His Val Gly						
305		310		315		320
Met Ser Ser Thr Glu Pro Val Ile Asn Thr Tyr Ala Asn Phe Arg Asp						
	325			330		335
Asp Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala Val Gln Leu						
	340			345		350
Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val						
	355			360		365
Thr Asn Phe Tyr Ala Ala Ser Ser Arg Phe Gly Thr Pro Asp Asp Leu						
	370			375		380
Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu Leu Val Leu Met						
385		390		395		400
Asp Ile Val His Ser His Ala Ser Thr Asn Thr Leu Asp Gly Leu Asn						
	405			410		415
Met Phe Asp Gly Thr Asp Gly His Tyr Phe His Ser Gly Pro Arg Gly						
	420			425		430
His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Ser Trp Glu						
	435			440		445
Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Asp Glu Tyr						
	450			455		460
Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr						
465		470		475		480
His His Gly Leu Gln Val Asp Phe Thr Gly Asn Tyr Asn Glu Tyr Phe						
	485			490		495
Gly Tyr Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Leu Asn						
	500			505		510
Asp Met Ile His Gly Leu Phe Pro Glu Ala Val Thr Ile Gly Glu Asp						
	515			520		525
Val Ser Gly Met Pro Thr Val Cys Ile Pro Val Glu Asp Gly Gly Val						

530

535

540

Gly Phe Asp Tyr Arg Leu His Met Ala Val Ala Asp Lys Trp Val Glu  
545 550 555 560

Ile Ile Gln Lys Arg Asp Glu Asp Trp Lys Met Gly Asp Ile Val His  
565 570 575

Met Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Ser Tyr Ala Glu  
580 585 590

Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu  
595 600 605

Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr  
610 615 620

Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile  
625 630 635 640

Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu  
645 650 655

Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu  
660 665 670

Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys  
675 680 685

Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys His Leu Arg Tyr His Gly  
690 695 700

Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly  
705 710 715 720

Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp  
725 730 735

Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe  
740 745 750

His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro  
755 760 765

Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly  
770 775 780

Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp  
785 790 795 800

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr  
805 810 815

Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Leu Glu  
820 825 830

Pro Val Ala Gly \*

<210> SEQ ID NO: #30

<211> LENGTH: 3090 base pairs

<212> DNA

<213> genus, species

<220>

<221> CDS

<222> 131..2677

<223>

<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #30

AGTGAATTTCG AGCTCGGTAC CCGGGGATCC GATTCGCATT TCTCGCTATT GCTTTCCGTT 60

TATTTCCATA TATAAAATAT CAAATCTAAT CACTTGCGCC ATTTCTATCT CTCTCCAAAC 120

TCTCACCGAA ATG GTA TAC TAC ACT GTA TCA GGC ATA CGT TTT CCT TGT 169  
Met Val Tyr Tyr Thr Val Ser Gly Ile Arg Phe Pro Cys  
840 845 850

GCA CCT TCA CTC TAC AAA TCT CAG CTC ACC AGC TTC CAT GGC GGT CGA 217  
Ala Pro Ser Leu Tyr Lys Ser Gln Leu Thr Ser Phe His Gly Gly Arg



855	860	865	
AGG ACC TCT TCT GGC CTT TCC TTC CTC TTG AAG AAG GAG CTG TTT CCT Arg Thr Ser Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro 870 875 880			265
CGG AAG ATC TTT GCT GGA AAG TCC TCT TAT GAA TCT GAC TCC TCA AAT Arg Lys Ile Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn 885 890 895			313
TTA ACT GTC TCT GCA TCT GAG AAG GTC CTT GTT CCT GAT GAT CAG ATT Leu Thr Val Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile 900 905 910			361
GAT GGC TCT TCT TCT TCA ACA TAT CAA TTA GAA ACC ACT GGC ACA GTT Asp Gly Ser Ser Ser Ser Thr Tyr Gln Leu Glu Thr Thr Gly Thr Val 915 920 925 930			409
TTG GAG GAA TCC CAG GTT CTT GGT GAT GCA GAG AGT CTT GTG ATG GAA Leu Glu Glu Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu 935 940 945			457
GAT GAT AAG AAT GTT GAG GAG GAT GAA GTA AAA AAA GAG TCG GTT CCA Asp Asp Lys Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro 950 955 960			505
TTG CAT GAG ACA ATT AGC ATT GGA AAA AGT GAA TCT AAA CCA AGG TCC Leu His Glu Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser 965 970 975			553
ATT CCT CCA CCT GGC AGT GGG CAG AGA ATA TAT GAC ATA GAT CCA AGC Ile Pro Pro Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser 980 985 990			601
TTG GCA GGT TTC CGT CAG CAT CTT GAC TAC CGA TAT TCA CAG TAC AAA Leu Ala Gly Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys 995 1000 1005 1010			649
AGG CTG CGT GAG GAA ATT GAC AAG TAT GAA GGT GGT TTG GAT GCA TTC Arg Leu Arg Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe 1015 1020 1025			697
TCT CGT GGA TTT GAA AAG TTT GGT TTC TTA CGC AGT GAA ACA GGA ATA Ser Arg Gly Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile 1030 1035 1040			745
ACT TAT AGG GAA TGG GCA CCT GGA GCT ACG TGG GCT GCA CTT ATT GGA Thr Tyr Arg Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly 1045 1050 1055			793
GAT TTC AAC AAT TGG AAT CCT AAT GCA GAT GTC ATG ACT CGG AAT GAG Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu 1060 1065 1070			841
TTT GGT GTC TGG GAG ATT TTT TTG CCA AAT AAC GCA GAT GGT TCA CCA Phe Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro 1075 1080 1085 1090			889

CCA ATT CCT CAT GGT TCT CGA GTA AAG ATA CGC ATG GAT ACT CCA TCT Pro Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser 1095 1100 1105	937
GGC ATC AAA GAT TCA ATT CCT GCT TGG ATC AAG TTC TCA GTT CAG GCA Gly Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala 1110 1115 1120	985
CCT GGT GAA ATC CCA TAC AAT GCC ATA TAC TAT GAT CCA CCA AAG GAG Pro Gly Glu Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu 1125 1130 1135	1033
GAG AAG TAT GTG TTC AAA CAT CCT CAG CCA AAG AGA CCA AAA TCA CTT Glu Lys Tyr Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu 1140 1145 1150	1081
AGG ATT TAT GAA TCT CAT GTT GGG ATG AGT AGT ATG GAG CCA ATA ATT Arg Ile Tyr Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile 1155 1160 1165 1170	1129
AAC ACA TAT GCC AAC TTT AGA GAT GAT ATG CTT CCT CGC ATC AAA AAG Asn Thr Tyr Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys 1175 1180 1185	1177
CTT GGC TAC AAT GCT GTT CAG ATC ATG GCT ATT CAA GAG CAT TCC TAT Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr 1190 1195 1200	1225
TAT GCT AGT TTT GGG TAC CAT GTC ACA AAC TTT TTT GCA CCT AGC AGC Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser 1205 1210 1215	1273
CGA TTT GGA ACT CCT GAT GAT TTG AAG TCT TTA ATA GAT AAA GCT CAT Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His 1220 1225 1230	1321
GAG TTA GGG CTG CTT GTT CTC ATG GAT ATT GTT CAT AGC CAT GCG TCA Glu Leu Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser 1235 1240 1245 1250	1369
AAT AAT ACG TTG GAT GGG CTG AAC ATG TTT GAT GGT ACG GAT AGT CAC Asn Asn Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His 1255 1260 1265	1417
TAC TTC CAC TCC GGA TCA CGG GGT CAT CAT TGG TTG TGG GAC TCT CGC Tyr Phe His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg 1270 1275 1280	1465
CTT TTC AAC TAT GGA AGC TGG GAG GTG CTA AGA TTT CTT CTT TCA AAT Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn 1285 1290 1295	1513
GCA AGA TGG TGG TTG GAA GAG TAC AGG TTT GAT GGT TTT AGA TTT GAT Ala Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp 1300 1305 1310	1561

GGG GTG ACT TCC ATG ATG TAC ACT CCC CAT GGG TTG CAG GTA GCT TTT Gly Val Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe 1315 1320 1325 1330	1609
ACT GGC AAC TAC AAT GAG TAC TTT GGA TAT GCA ACT GAT GTA GAT GCT Thr Gly Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala 1335 1340 1345	1657
GTG ATT TAT TTG ATG CTT GTG AAT GAT ATG ATT CAC GGT CTT TTC CCT Val Ile Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro 1350 1355 1360	1705
GAG GCT GTT ACC ATT GGT GAA GAT GTT AGC GGA AAG CCA ACA TTT TGC Glu Ala Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys 1365 1370 1375	1753
ATT CCA GTG GAA GAT GGT GGT GTT GGA TTT GAT TAC CGT CTC CAC ATG Ile Pro Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met 1380 1385 1390	1801
GCC ATT GCC GAT AAA TGG ATT GAG ATT CTT AAG AAG AGA GAT GAG GAC Ala Ile Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp 1395 1400 1405 1410	1849
TGG AAA ATG GGT GAC ATT GTG CAT ACA CTC ACC AAC AGA AGG TGG TTG Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu 1415 1420 1425	1897
GAA AAA TGT GTT GCT TAT GCT GAA AGT CAT GAC CAA GCT CTT GTT GGT Glu Lys Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly 1430 1435 1440	1945
GAC AAA ACT ATT GCA TTT TGG CTG ATG GAC AAG GAC ATG TAC GAC TTC Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe 1445 1450 1455	1993
ATG GCT CGT GAC AGA CCA TCT ACT CCT CTT ATA GAT CGT GGA ATA GCA Met Ala Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala 1460 1465 1470	2041
TTG CAC AAA ATG ATC AGG CTT ATT ACC ATG GGC TTA GGC GGA GAA GGA Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly 1475 1480 1485 1490	2089
TAT TTG AAT TTT ATG GGA AAT GAA TTT GGA CAT CCT GAG TGG ATT GAT Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp 1495 1500 1505	2137
TTT CCA AGA GGG GAT CGA CAT CTG CCC AAT GGT AAA GTA ATT CCA GGG Phe Pro Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly 1510 1515 1520	2185
AAC AAC CAC AGT TAT GAT AAA TGC CGT CGT AGA TTT GAT CTA GGT GAT Asn Asn His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp 1525 1530 1535	2233
GCA GAC TAT CTA AGA TAT CAT GGA ATG CAA GAG TTT GAT CAG GCA ATG	2281

Ala Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met 1540	1545	1550	
CAA CAT CTT GAA GAA GCC TAT GGT TTC ATG ACT TCT GAG CAC CAG TAT Gln His Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr 1555	1560	1565	2329
ATA TCA CGG AAG GAT GAA GGA GAT CGG ATC ATT GTC TTT GAG AGG GGA Ile Ser Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly 1575	1580	1585	2377
AAC CTT GTT TTT GTA TTC AAC TTT CAT TGG ACT AAC AGC TAT TCA GAT Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp 1590	1595	1600	2425
TAC CGA GTT GGC TGC TTC AAG TCA GGA AAG TAC AAG ATT GTT TTG GAC Tyr Arg Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp 1605	1610	1615	2473
TCG GAT GAT GGC TTG TTT GGA GGC TTC AAC AGG CTT AGT CAT GAT GCC Ser Asp Asp Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala 1620	1625	1630	2521
GAG CAC TTC ACC TTT GAC GGG TGG TAT GAT AAC CGG CCT CGG TCC TTC Glu His Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe 1635	1640	1645	2569
ATG GTA TAT GCA CCA TCT AGG ACA GCA GTG GTC TAT GCT TTA GTA GAA Met Val Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu 1655	1660	1665	2617
GAT GAA GAG AAT GAA GCA GAG AAT GAA GTA GAA AGT GAA GTG AAA CCA Asp Glu Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro 1670	1675	1680	2665
GCC TCC GGC TGA GATAGATATT TAGTAAGAGG ATCCCCTAAA GCAGGAATGG Ala Ser Gly * 1685			2717
TTAACCTGTG CATCTGCATT GAACGACGTA TATTGAGACT TGAATTGATT TGCTGCTCAG			2777
GACACAGAAT ATTAATTCCA AGGCTCAAGG CAGAGATACA CGCCATAATG CATGATCATA			2837
TGAAAGCTCC CCAACTTGTA AATCATTTAG CAAGCTGCGT GCACTCTGTA AATTATATGT			2897
AGTACTTTGG CAAGTCACGT TATTATGGAT ACCATGGATG TCCGCTAGGA AAAATTTTGT			2957
GTATACGCCT ACTAGGATTT TTAAATCTCG CATGTTCCAC ATAAAGTGGT GGTTGAATGT			3017
TGCGCGACTA TTTTGTAGTA AAATGATTGA AGTTATTCTT CACTTGGGCC TGTGAAAAAA			3077
AAAAAAAAAA AAA			3090
<210> SEQ ID NO: #31			
<211> LENGTH: 849 amino acids			

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #31

Met Val Tyr Tyr Thr Val Ser Gly Ile Arg Phe Pro Cys Ala Pro Ser  
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Leu Tyr Lys Ser Gln Leu Thr Ser Phe His Gly Gly Arg Arg Thr Ser  
20 25 30

Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro Arg Lys Ile  
35 40 45

Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn Leu Thr Val  
50 55 60

Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile Asp Gly Ser  
65 70 75 80

Ser Ser Ser Thr Tyr Gln Leu Glu Thr Thr Gly Thr Val Leu Glu Glu

85

90

95

Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu Asp Asp Lys  
 100 105 110

Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro Leu His Glu  
 115 120 125

Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser Ile Pro Pro  
 130 135 140

Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser Leu Ala Gly  
 145 150 155 160

Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu Arg  
 165 170 175

Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe Ser Arg Gly  
 180 185 190

Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile Thr Tyr Arg  
 195 200 205

Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe Asn  
 210 215 220

Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu Phe Gly Val  
 225 230 235 240

Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro  
 245 250 255

His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Ile Lys  
 260 265 270

Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu  
 275 280 285

Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu Glu Lys Tyr  
 290 295 300

Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr  
 305 310 315 320

Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile Asn Thr Tyr  
 325 330 335

Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys Leu Gly Tyr  
 340 345 350

Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser  
 355 360 365

Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly  
 370 375 380

Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly

385	390	395	400
Leu Leu Val	Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn Thr		
	405	410	415
Leu Asp Gly	Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe His		
	420	425	430
Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe Asn			
	435	440	445
Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp			
	450	455	460
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr			
	465	470	475
Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly Asn			
	485	490	495
Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile Tyr			
	500	505	510
Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala Val			
	515	520	525
Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro Val			
	530	535	540
Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile Ala			
	545	550	555
Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys Met			
	565	570	575
Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys			
	580	585	590
Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr			
	595	600	605
Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Arg			
	610	615	620
Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys			
	625	630	635
Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn			
	645	650	655
Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg			
	660	665	670
Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn His			
	675	680	685
Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr			

690

695

700

Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu  
 705 710 715 720

Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg  
 725 730 735

Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val  
 740 745 750

Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Val  
 755 760 765

Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp  
 770 775 780

Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His Phe  
 785 790 795 800

Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr  
 805 810 815

Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu Asp Glu Glu  
 820 825 830

Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser Gly  
 835 840 845

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<210> SEQ ID NO: #32

<211> LENGTH: 48 base pairs

<212> DNA

<213> genus, species

<220>

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #32

GGAAATCCAT ATGACTAGTA GATCCTCTAG AGTCGACCTG CAGGCATG

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<210> SEQ ID NO: #33

<211> LENGTH: 1069 base pairs

<212> DNA

<213> genus, species

<220>

<221> CDS

<222> 1..687

<223>

<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #33

ATG GAC AAG GAT ATG TAT GAC TTC ATG GCT CTT GAC AGA CCA TCT ACT	48
Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr	
1 5 10 15	
CCT CTC ATA GAT CGT GGA GTA GCA TTG CAC AAA ATG ATC AGG CTT ATT	96
Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile	
20 25 30	
ACC ATG GGA TTA GGC GGA GAA GGA TAT TTG AAT TTT ATG GGA AAT GAA	144
Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu	
35 40 45	
TTT GGA CAC CCC GAG TGG ATT GAT TTT CCA AGA GGT GAT CTA CAT CTT	192
Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu	
50 55 60	
CCC AGT GGT AAA TTT GTT CCT GGG AAC AAT TAC AGT TAT GAT AAA TGC	240
Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys	
65 70 75 80	
CGG CGT AGG TTT GAT CTA GGC AAT TCA AAG CGT CTG AGA TAT CAT GGA	288
Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly	
85 90 95	
ATG CAA GAG TTT GAT CAA GCA ATT CAG CAT CTT GAA GAA GCC TAT GGT	336
Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly	
100 105 110	
TTC ATG ACT TCT GAG CAC CAA TAC ATA TCA CGG AAG GAT GAA AGG GAT	384
Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp	
115 120 125	
CGG ATC ATT GTC TTC GAG AGG GGA AAC CTC GTT TTT GTA TTC AAT TTT	432
Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe	
130 135 140	
CAT TGG ACT AGC AGC TAT TCG GAT TAC CGA GTT GGC TGC TTA AAG CCA	480
His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro	
145 150 155 160	
GGA AAG TAC AAG ATA GTC TTG GAT TCA GAT GAT CCT TTG TTT GGA GGC	528
Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly	
165 170 175	
TTT GGC AGG CTT AGT CAT GAT GCA GAG CAC TTC AGC TTT GAA GGG TGG	576
Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp	
180 185 190	
TAC GAT AAC CGG CCT CGA TCC TTC ATG GTG TAC ACA CCA TGT AGA ACA	624

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr  
 195 200 205

GCA GTG GTC TAT GCT TTA GTG GAG GAT GAA GTG GAG AAT GAA GTG GAA 672  
 Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu  
 210 215 220

CCT GTC GCC GGT TAA GATATATCTT AGCAACAGGT TCTGAAGCAG GAATGCCATT 727  
 Pro Val Ala Gly \*  
 225

ATTGATCTTC CTATGTGCAT CTGCGTTGAA CGAAATATAT TGAGCCTATA ATTTGATGTC 787

ACGGTCCTTG CAGATTTCCA TCCTGGTTCT TGGTATTTTG TTGTCATGAT AAACATAATC 847

AAAGACCAAT AGGAAACGCA GGGTTACATG CTAGCTTCCA TCATCATAGG GAGCTCAGAC 907

CTCCTAAACC ATAAATCTTC AAGCTGCCTG CGTTCGGTAG TATGTTATGT GGTACTTTGC 967

AATCTTAAAT TATCATGATC GCTGTGGATG CTAACATGA CAATTTTGTA TATATGCCAA 1027

CGAGGATTTT AAGTTTAAAA AAAAAACAA AAAAAATCCA TG 1069

<210> SEQ ID NO: #34

<211> LENGTH: 229 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #34

Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr  
1 5 10 15

Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile  
20 25 30

Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu  
35 40 45

Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu  
50 55 60

Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys  
65 70 75 80

Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly  
85 90 95

Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly  
100 105 110

Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp  
115 120 125

Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe  
130 135 140

His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro  
145 150 155 160

Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly  
165 170 175

Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp  
180 185 190

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr  
195 200 205

Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu  
210 215 220

Pro Val Ala Gly \*  
225

<210> SEQ ID NO: #35

<211> LENGTH: 1919 base pairs

<212> DNA

<213> genus, species

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<221> CDS

<222> 61..1506

<223>

<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #35

TATGGATTGA CATCGATAAT ACGACTCACT ATAGGGATTT TTTTTTTTTT TTTTTTTTGT 60

AGT TTT GGG TAC CAT GTC ACA AAC TTT TTT GCA CCT AGC AGC CGA TTT 108  
Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe  
230 235 240 245

GGA ACT CCT GAT GAT TTG AAG TCT TTA ATA GAT AAA GCT CAT GAG TTA 156  
Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu  
250 255 260

GGG CTG CTT GTT CTC ATG GAT ATT GTT CAT AGC CAT GCG TCA AAT AAT 204  
Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn  
265 270 275

ACG TTG GAT GGG CTG AAC ATG TTT GAT GGT ACG GAT AGT CAC TAC TTC Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe 280 285 290	252
CAC TCC GGA TCA CGG GGT CAT CAT TGG TTG TGG GAC TCT CGC CTT TTC His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe 295 300 305	300
AAC TAT GGA AGC TGG GAG GTG CTA AGA TTT CTT CTT TCA AAT GCA AGA Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg 310 315 320 325	348
TGG TGG TTG GAA GAG TAC AGG TTT GAT GGT TTT AGA TTT GAT GGG GTG Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val 330 335 340	396
ACT TCC ATG ATG TAC ACT CCC CAT GGG TTG CAG GTA GCT TTT ACT GGC Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly 345 350 355	444
AAC TAC AAT GAG TAC TTT GGA TAT GCA ACT GAT GTA GAT GCT GTG ATT Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile 360 365 370	492
TAT TTG ATG CTT GTG AAT GAT ATG ATT CAC GGT CTT TTC CCT GAG GCT Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala 375 380 385	540
GTT ACC ATT GGT GAA GAT GTT AGC GGA AAG CCA ACA TTT TGC ATT CCA Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro 390 395 400 405	588
GTG GAA GAT GGT GGT GTT GGA TTT GAT TAC CGT CTC CAC ATG GCC ATT Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile 410 415 420	636
GCC GAT AAA TGG ATT GAG ATT CTT AAG AAG AGA GAT GAG GAC TGG AAA Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys 425 430 435	684
ATG GGT GAC ATT GTG CAT ACA CTC ACC AAC AGA AGG TGG TTG GAA AAA Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys 440 445 450	732
TGT GTT GCT TAT GCT GAA AGT CAT GAC CAA GCT CTT GTT GGT GAC AAA Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys 455 460 465	780
ACT ATT GCA TTT TGG CTG ATG GAC AAG GAC ATG TAC GAC TTC ATG GCT Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala 470 475 480 485	828
CGT GAC AGA CCA TCT ACT CCT CTT ATA GAT CGT GGA ATA GCA TTG CAC Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His 490 495 500	876

AAA ATG ATC AGG CTT ATT ACC ATG GGC TTA GGC GGA GAA GGA TAT TTG Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu 505 510 515	924
AAT TTT ATG GGA AAT GAA TTT GGA CAT CCT GAG TGG ATT GAT TTT CCA Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro 520 525 530	972
AGA GGG GAT CGA CAT CTG CCC AAT GGT AAA GTA ATT CCA GGG AAC AAC Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn 535 540 545	1020
CAC AGT TAT GAT AAA TGC CGT CGT AGA TTT GAT CTA GGT GAT GCA GAC His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp 550 555 560 565	1068
TAT CTA AGA TAT CAT GGA ATG CAA GAG TTT GAT CAG GCA ATG CAA CAT Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His 570 575 580	1116
CTT GAA GAA GCC TAT GGT TTC ATG ACT TCT GAG CAC CAG TAT ATA TCA Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser 585 590 595	1164
CGG AAG GAT GAA GGA GAT CGG ATC ATT GTC TTT GAG AGG GGA AAC CTT Arg Lys Asp Glu Gly Asp Arg Ile Val Phe Glu Arg Gly Asn Leu 600 605 610	1212
GTT TTT GTA TTC AAC TTT CAT TGG ACT AAC AGC TAT TCA GAT TAC CGA Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg 615 620 625	1260
GTT GGC TGC TTC AAG TCA GGA AAG TAC AAG ATT GTT TTG GAC TCG GAT Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp 630 635 640 645	1308
GAT GGC TTG TTT GGA GGC TTC AAC AGG CTT AGT CAT GAT GCC GAG CAC Asp Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His 650 655 660	1356
TTC ACC TTT GAC GGG TGG TAT GAT AAC CGG CCT CGG TCC TTC ATG GTA Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val 665 670 675	1404
TAT GCA CCA TCT AGG ACA GCA GTG GTC CAT GCT TTA GTA GAA GAT GAA Tyr Ala Pro Ser Arg Thr Ala Val Val His Ala Leu Val Glu Asp Glu 680 685 690	1452
GAG AAT GAA GCA GAG AAT GAA GTA GAA AGT GAA GTG AAA CCA GCC TCC Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser 695 700 705	1500
GGC TGA GATAGATATT TAGTAAGAGG ATCCCCTAAA GCAGGAATGG TTAACCTGTG Gly * 710	1556
CATCTGCATT GAACGACGTA TATTGAGACT TGAATTGATT TGCTGCTCAG GACACAGAAT	1616

ATTAATTCCA AGGCTCAAGG CAGAGATACA CGCCATAATG CATGATCATA TGAAAGCTCC 1676  
CCAACCTTGTA AATCATTAG CAAGCTGCGT GCACTCTGTA AATTATATGT AGTACTTTGG 1736  
CAAGTCACGT TATTATGGAT ACCATGGATG TCCGCTAGGA AAAATTTTGT GTATACGCCT 1796  
ACTAGGATTT TTAAATCTCG CATGTTCCAC ATAAAGTGGT GGTGAATGT TGCGCGACTA 1856  
TTTTTGAGTA AAATGATTGA AGTTATTCTT CACTTGGGCC TGTGAAAAAA AAAAAAAAAA 1916  
AAA 1919

<210> SEQ ID NO: #36

<211> LENGTH: 482 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #36

Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe  
1 5 10 15

Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu  
20 25 30

Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn  
35 40 45

Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe  
50 55 60

His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe  
65 70 75 80

Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg  
85 90 95

Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val  
100 105 110

Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly  
115 120 125

Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile  
130 135 140

Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala  
145 150 155 160

Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro  
165 170 175

Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile  
180 185 190

Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys  
195 200 205

Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys  
210 215 220

Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys  
225 230 235 240

Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala  
245 250 255

Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His  
260 265 270

Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu  
275 280 285

Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro  
290 295 300

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Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn  
 305 310 315 320  
 His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp  
 325 330 335  
 Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His  
 340 345 350  
 Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser  
 355 360 365  
 Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu  
 370 375 380  
 Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg  
 385 390 395 400  
 Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp  
 405 410 415  
 Asp Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His  
 420 425 430  
 Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val  
 435 440 445  
 Tyr Ala Pro Ser Arg Thr Ala Val Val His Ala Leu Val Glu Asp Glu  
 450 455 460  
 Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser  
 465 470 475 480

Gly \*